



1600

RAW SEQUENCE LISTING

DATE: 02/03/2003

PATENT APPLICATION: US/09/875,321A

TIME: 09:15:39

Input Set : A:\Sequence listing.TXT

Output Set: N:\CRF4\02032003\I875321A.raw

4 <110> APPLICANT: Curtis, Rory A.J.
6 <120> TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM
7 CHANNEL FAMILY MEMBERS AND USES THEREOF
10 <130> FILE REFERENCE: 10448-061001
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,321A
C--> 12 <141> CURRENT FILING DATE: 2000-06-06
12 <150> PRIOR APPLICATION NUMBER: US 60/209,845
13 <151> PRIOR FILING DATE: 2000-06-06
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3525
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (638)...(3178)
28 <400> SEQUENCE: 1

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30	tcccgcagcg gccaaaggcag ggctcaggcc ccgggattct ccccacacgc tgctgcaactg	120
31	gcgcagcccg tcgccaaact ttttctcccc aaagccagtg ccccgagctg tacttgccgg	180
32	gcagccggca gccactctc ggccgggatga tctgggagaa gcgggctgg gacgaggggg	240
33	ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggctcgggg tccacaccgt	300
34	ccctgagcct gcccctggc caaggtggcc cgacgtgctg cagtggctgg cgcaggtgat	360
35	ccgggcagcg cgtccggcac tagtcaagg ggagcggca cgggaggag gggcgcttt	420
36	ctcttttctc ctcccctgc agcccagctg cactgcgtgg gggtctcca tctccacgca	480
37	atcagcaggc ggaatccctg ccctggagcg ccctggctct ggactgcacc cccctaggg	540
38	ttgtcctgca gattctctc cccatctttc tctgccacac acgcttcctt aagccgcgcg	600
39	cgccgcaaac tcagtctcgg tccccgcagg tgatgtc atg ccc att gtt ttg gtg	655
40	Met Pro Ile Val Leu Val	
41	1 5	
43	cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg	703
44	Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp Ser Thr Gly Ala Gly Met	
45	10 15 20	
47	ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg	751
48	Gly Pro Ser Ser His Gln Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr	
49	25 30 35	
51	cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac agc	799
52	His Cys Ala Gly Cys Thr Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser	
53	40 45 50	
55	cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag	847
56	Pro Asp Met Glu Thr Pro Leu Gln Phe Gln Arg Gly Phe Phe Pro Glu	
57	55 60 65 70	

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59	cag	ccg	ccg	ccg	ccg	ccg	ccg	cgc	tcc	tca	cac	ctg	cat	tgc	cag	cag	cag	895
60	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Ser	Ser	His	Leu	His	Cys	Gln	Gln	Gln	
61						75					80					85		
63	caa	cag	agc	cag	gac	aag	ccg	tgc	ccg	ccc	ttc	gcg	ccc	ctc	ccg	cac	943	
64	Gln	Gln	Ser	Gln	Asp	Lys	Pro	Cys	Pro	Pro	Phe	Ala	Pro	Leu	Pro	His		
65				90					95					100				
67	cct	cac	cac	cac	ccg	cac	ctc	gcg	cac	cag	cag	ccg	gcc	agc	ggc	ggc	991	
68	Pro	His	His	His	Pro	His	Leu	Ala	His	Gln	Gln	Pro	Ala	Ser	Gly	Gly		
69			105					110					115					
71	agc	agc	cca	tgc	ctc	cgg	tgc	aac	agc	tgc	gcc	tcc	tcc	ggg	gcc	ccg	1039	
72	Ser	Ser	Pro	Cys	Leu	Arg	Cys	Asn	Ser	Cys	Ala	Ser	Ser	Gly	Ala	Pro		
73		120					125					130						
75	gcg	gcg	ggg	gcg	gga	gat	aac	ctg	tcc	ctg	ctg	ctc	cgc	acc	tcc	tcg	1087	
76	Ala	Ala	Gly	Ala	Gly	Asp	Asn	Leu	Ser	Leu	Leu	Leu	Arg	Thr	Ser	Ser		
77	135					140					145					150		
79	ccc	ggc	ggc	gcc	ttc	cgg	acc	cgc	acc	tcc	tcg	ccg	ctg	tcg	ggc	tcg	1135	
80	Pro	Gly	Gly	Ala	Phe	Arg	Thr	Arg	Thr	Ser	Ser	Pro	Leu	Ser	Gly	Ser		
81				155				160					165					
83	tcc	tgc	tgc	tgc	tgc	tgc	tgc	tcg	tcg	cgc	cgg	ggc	agc	cag	ctc	aat	1183	
84	Ser	Cys	Cys	Cys	Cys	Cys	Cys	Ser	Ser	Arg	Arg	Gly	Ser	Gln	Leu	Asn		
85			170					175					180					
87	gtg	agc	gag	ctg	acg	ccg	tcc	agc	cat	gcc	agt	gcg	ctc	cgg	cag	cag	1231	
88	Val	Ser	Glu	Leu	Thr	Pro	Ser	Ser	His	Ala	Ser	Ala	Leu	Arg	Gln	Gln		
89			185					190					195					
91	tac	gcg	cag	cag	tcc	gcg	cag	cag	tcg	gcg	tcc	gcc	tcc	cag	tac	cac	1279	
92	Tyr	Ala	Gln	Gln	Ser	Ala	Gln	Gln	Ser	Ala	Ser	Ala	Ser	Gln	Tyr	His		
93		200					205					210						
95	cag	tgc	cac	agc	ctg	cag	ccc	gcc	gcc	agc	ccc	acg	ggc	agc	ctc	ggc	1327	
96	Gln	Cys	His	Ser	Leu	Gln	Pro	Ala	Ala	Ser	Pro	Thr	Gly	Ser	Leu	Gly		
97	215					220					225				230			
99	agt	ctg	ggc	tcc	ggg	ccc	ccg	ctc	tcg	cac	cac	cac	cac	cac	ccg	cac	1375	
100	Ser	Leu	Gly	Ser	Gly	Pro	Pro	Leu	Ser	His	His	His	His	His	Pro	His		
101				235						240			245					
103	ccg	gcg	cac	cac	cag	cac	cac	cag	ccc	cag	gcg	cgc	cgc	gag	agc	aac	1423	
104	Pro	Ala	His	His	Gln	His	His	Gln	Pro	Gln	Ala	Arg	Arg	Glu	Ser	Asn		
105				250					255				260					
107	ccc	ttc	acc	gaa	ata	gcc	atg	agc	agc	tgc	agg	tac	aac	ggg	ggc	gtc	1471	
108	Pro	Phe	Thr	Glu	Ile	Ala	Met	Ser	Ser	Cys	Arg	Tyr	Asn	Gly	Gly	Val		
109			265					270					275					
111	atg	cgg	ccg	ctc	agc	aac	ttg	agc	gcg	tcc	cgc	cgg	aac	ctg	cac	gag	1519	
112	Met	Arg	Pro	Leu	Ser	Asn	Leu	Ser	Ala	Ser	Arg	Arg	Asn	Leu	His	Glu		
113		280					285					290						
115	atg	gac	tca	gag	gcg	cag	ccc	ctg	cag	ccc	ccc	gcg	tct	gtc	gga	gga	1567	
116	Met	Asp	Ser	Glu	Ala	Gln	Pro	Leu	Gln	Pro	Pro	Ala	Ser	Val	Gly	Gly		
117	295					300					305				310			
119	ggg	ggc	ggc	gcg	tcc	tcc	ccg	tct	gca	gcc	gct	gcc	gcc	gcc	gcc	gct	1615	
120	Gly	Gly	Gly	Ala	Ser	Ser	Pro	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala		
121				315					320				325					
123	gtt	tcg	tcc	tca	gcc	ccc	gag	atc	gtg	gtg	tct	aag	ccc	gag	cac	aac	1663	

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124	Val	Ser	Ser	Ser	Ala	Pro	Glu	Ile	Val	Val	Ser	Lys	Pro	Glu	His	Asn	
125				330					335					340			
127	aac	tcc	aac	aac	ctg	gcg	ctc	tat	gga	acc	ggc	ggc	gga	ggc	agc	act	1711
128	Asn	Ser	Asn	Asn	Leu	Ala	Leu	Tyr	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Thr	
129			345					350						355			
131	gga	gga	ggc	ggc	ggc	ggt	ggc	ggg	agc	ggg	cac	ggc	agc	agc	agt	ggc	1759
132	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	His	Gly	Ser	Ser	Ser	Gly	
133		360						365						370			
135	acc	aag	tcc	agc	aaa	aag	aaa	aac	cag	aac	atc	ggc	tac	aag	ctg	ggc	1807
136	Thr	Lys	Ser	Ser	Lys	Lys	Lys	Asn	Gln	Asn	Ile	Gly	Tyr	Lys	Leu	Gly	
137	375					380					385					390	
139	cac	cgg	cgc	gcc	ctg	ttc	gaa	aag	cgc	aag	cgg	ctc	agc	gac	tac	gcg	1855
140	His	Arg	Arg	Ala	Leu	Phe	Glu	Lys	Arg	Lys	Arg	Leu	Ser	Asp	Tyr	Ala	
141				395						400					405		
143	ctc	atc	ttc	ggc	atg	ttc	ggc	atc	gtg	gtc	atg	gtc	atc	gag	acc	gag	1903
144	Leu	Ile	Phe	Gly	Met	Phe	Gly	Ile	Val	Val	Met	Val	Ile	Glu	Thr	Glu	
145			410					415						420			
147	ctg	tcg	tgg	ggc	gcc	tac	gac	aag	gcg	tcg	ctg	tat	tcc	tta	gct	ctg	1951
148	Leu	Ser	Trp	Gly	Ala	Tyr	Asp	Lys	Ala	Ser	Leu	Tyr	Ser	Leu	Ala	Leu	
149			425					430						435			
151	aaa	tgc	ctt	atc	agt	ctc	tcc	acg	atc	atc	ctg	ctc	ggt	ctg	atc	atc	1999
152	Lys	Cys	Leu	Ile	Ser	Leu	Ser	Thr	Ile	Ile	Leu	Leu	Gly	Leu	Ile	Ile	
153		440						445					450				
155	gtg	tac	cac	gcc	agg	gaa	ata	cag	ttg	ttc	atg	gtg	gac	aat	gga	gca	2047
156	Val	Tyr	His	Ala	Arg	Glu	Ile	Gln	Leu	Phe	Met	Val	Asp	Asn	Gly	Ala	
157	455					460				465					470		
159	gat	gac	tgg	aga	ata	gcc	atg	act	tat	gag	cgt	att	ttc	ttc	atc	tgc	2095
160	Asp	Asp	Trp	Arg	Ile	Ala	Met	Thr	Tyr	Glu	Arg	Ile	Phe	Phe	Ile	Cys	
161				475					480					485			
163	ttg	gaa	ata	ctg	gtg	tgt	gct	att	cat	ccc	ata	cct	ggg	aat	tat	aca	2143
164	Leu	Glu	Ile	Leu	Val	Cys	Ala	Ile	His	Pro	Ile	Pro	Gly	Asn	Tyr	Thr	
165			490					495						500			
167	ttc	aca	tgg	acg	gcc	cgg	ctt	gcc	ttc	tcc	tat	gcc	cca	tcc	aca	acc	2191
168	Phe	Thr	Trp	Thr	Ala	Arg	Leu	Ala	Phe	Ser	Tyr	Ala	Pro	Ser	Thr	Thr	
169			505					510						515			
171	acc	gct	gat	gtg	gat	att	att	tta	tct	ata	cca	atg	ttc	tta	aga	ctc	2239
172	Thr	Ala	Asp	Val	Asp	Ile	Ile	Leu	Ser	Ile	Pro	Met	Phe	Leu	Arg	Leu	
173		520						525					530				
175	tat	ctg	att	gcc	aga	gtc	atg	ctt	tta	cat	agc	aaa	ctt	ttc	act	gat	2287
176	Tyr	Leu	Ile	Ala	Arg	Val	Met	Leu	Leu	His	Ser	Lys	Leu	Phe	Thr	Asp	
177	535					540					545				550		
179	acc	tcc	tct	aga	agc	att	gga	gca	ctt	aat	aag	ata	aac	ttc	aat	aca	2335
180	Thr	Ser	Ser	Arg	Ser	Ile	Gly	Ala	Leu	Asn	Lys	Ile	Asn	Phe	Asn	Thr	
181				555						560				565			
183	cgt	ttt	gtt	atg	aag	act	tta	atg	act	ata	tgc	cca	gga	act	gta	ctc	2383
184	Arg	Phe	Val	Met	Lys	Thr	Leu	Met	Thr	Ile	Cys	Pro	Gly	Thr	Val	Leu	
185			570					575						580			
187	ttg	gtt	ttt	agt	atc	tca	tta	tgg	ata	att	gcc	gca	tgg	act	gtc	cga	2431
188	Leu	Val	Phe	Ser	Ile	Ser	Leu	Trp	Ile	Ile	Ala	Ala	Trp	Thr	Val	Arg	

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189				585				590				595								
191	gct	tgt	gaa	agg	tac	cat	gat	caa	cag	gat	gtt	act	agc	aac	ttc	ctt		2479		
192	Ala	Cys	Glu	Arg	Tyr	His	Asp	Gln	Gln	Asp	Val	Thr	Ser	Asn	Phe	Leu				
193	600							605				610								
195	gga	gcg	atg	tgg	ttg	ata	tca	ata	act	ttt	ctc	tcc	att	ggg	tat	ggg		2527		
196	Gly	Ala	Met	Trp	Leu	Ile	Ser	Ile	Thr	Phe	Leu	Ser	Ile	Gly	Tyr	Gly				
197	615							620				625				630				
199	gac	atg	gta	cct	aac	aca	tac	tgt	gga	aaa	gga	gtc	tgc	tta	ctt	act		2575		
200	Asp	Met	Val	Pro	Asn	Thr	Tyr	Cys	Gly	Lys	Gly	Val	Cys	Leu	Leu	Thr				
201				635								640				645				
203	gga	att	atg	ggg	gct	ggg	tgc	aca	gcc	ctg	gtg	gta	gct	gta	gtg	gca		2623		
204	Gly	Ile	Met	Gly	Ala	Gly	Cys	Thr	Ala	Leu	Val	Val	Ala	Val	Val	Ala				
205				650								655				660				
207	agg	aag	cta	gaa	ctt	acc	aaa	gca	gaa	aaa	cac	gtg	cac	aat	ttc	atg		2671		
208	Arg	Lys	Leu	Glu	Leu	Thr	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe	Met				
209	665							670				675								
211	atg	gat	act	cag	ctg	act	aaa	aga	gta	aaa	aat	gca	gct	gcc	aat	gta		2719		
212	Met	Asp	Thr	Gln	Leu	Thr	Lys	Arg	Val	Lys	Asn	Ala	Ala	Ala	Asn	Val				
213	680							685				690								
215	ctc	agg	gaa	aca	tgg	cta	att	tac	aaa	aat	aca	aag	cta	gtg	aaa	aag		2767		
216	Leu	Arg	Glu	Thr	Trp	Leu	Ile	Tyr	Lys	Asn	Thr	Lys	Leu	Val	Lys	Lys				
217	695							700				705				710				
219	ata	gat	cat	gca	aaa	gta	aga	aaa	cat	caa	cga	aaa	ttc	ctg	caa	gct		2815		
220	Ile	Asp	His	Ala	Lys	Val	Arg	Lys	His	Gln	Arg	Lys	Phe	Leu	Gln	Ala				
221				715								720				725				
223	att	cat	caa	tta	aga	agt	gta	aaa	atg	gag	cag	agg	aaa	ctg	aat	gac		2863		
224	Ile	His	Gln	Leu	Arg	Ser	Val	Lys	Met	Glu	Gln	Arg	Lys	Leu	Asn	Asp				
225				730								735				740				
227	caa	gca	aac	act	ttg	gtg	gac	ttg	gca	aag	acc	cag	aac	atc	atg	tat		2911		
228	Gln	Ala	Asn	Thr	Leu	Val	Asp	Leu	Ala	Lys	Thr	Gln	Asn	Ile	Met	Tyr				
229	745							750				755								
231	gat	atg	att	tct	gac	tta	aac	gaa	agg	agt	gaa	gac	ttc	gag	aag	agg		2959		
232	Asp	Met	Ile	Ser	Asp	Leu	Asn	Glu	Arg	Ser	Glu	Asp	Phe	Glu	Lys	Arg				
233	760							765				770								
235	att	gtt	acc	ctg	gaa	aca	aaa	cta	gag	act	ttg	att	ggg	agc	atc	cac		3007		
236	Ile	Val	Thr	Leu	Glu	Thr	Lys	Leu	Glu	Thr	Leu	Ile	Gly	Ser	Ile	His				
237	775							780				785				790				
239	gcc	ctc	cct	ggg	ctc	ata	agc	cag	acc	atc	agg	cag	cag	cag	aga	gat		3055		
240	Ala	Leu	Pro	Gly	Leu	Ile	Ser	Gln	Thr	Ile	Arg	Gln	Gln	Gln	Arg	Asp				
241				795																

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255 acaaaataag actttttgcc atcatatggt caatatttta gctttttattg taaagcccct 3258
256 atggtttctaa tcagcggttat ccgggttctg atgtcagaat cctgggaacc tgaacactaa 3318
257 gtttttaggcc aaaatgagtg aaaactcttt ttttttcttt cagatgcaca gggaatgcac 3378
258 ctattattgc tatatagatt gttcctcctg taatttcact aactttttat tcatgcactt 3438
259 caaacaact ttactactac attatatgat atataataaa aaaagttaat ttctgcaaaa 3498
260 aaaaaaaaaa aaaaaaaaaa ggacggg 3525
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 847
264 <212> TYPE: PRT
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267 <400> SEQUENCE: 2
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270 Ser Thr Gly Ala Gly Met Gly Pro Ser Ser His Gln Gln Gln Glu Ser
271 20 25 30
272 Pro Leu Pro Thr Ile Thr His Cys Ala Gly Cys Thr Thr Ala Trp Ser
273 35 40 45
274 Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln
275 50 55 60
276 Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Pro Arg Ser Ser His
277 65 70 75 80
278 Leu His Cys Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro
279 85 90 95
280 Phe Ala Pro Leu Pro His Pro His His Pro His Leu Ala His Gln
281 100 105 110
282 Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys
283 115 120 125
284 Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu
285 130 135 140
286 Leu Leu Arg Thr Ser Ser Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser
287 145 150 155 160
288 Ser Pro Leu Ser Gly Ser Ser Cys Cys Cys Cys Cys Cys Ser Ser Arg
289 165 170 175
290 Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala
291 180 185 190
292 Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala
293 195 200 205
294 Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser
295 210 215 220
296 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His
297 225 230 235 240
298 His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln
299 245 250 255
300 Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys
301 260 265 270
302 Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser
303 275 280 285
304 Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln Pro Leu Gln Pro
305 290 295 300

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date